

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Seed, Brian et al.
- (ii) TITLE OF INVENTION: Targeted Cytolysis of HIV-Infected Cells by
Chimeric CD4 Receptor-Bearing Cells
- (iii) NUMBER OF SEQUENCES: 27
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Fish & Richardson
 - (B) STREET: 225 Franklin Street
 - (C) CITY: Boston
 - (D) STATE: MA
 - (E) COUNTRY: USA
 - (F) ZIP: 02110-2804
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 - (B) COMPUTER: IBM PS/2 Model 50Z or 55SX
 - (C) OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
 - (D) SOFTWARE: Wordperfect (Version 5.0)
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/847,566
 - (B) FILING DATE: March 6, 1992
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/665,961
 - (B) FILING DATE: March 7, 1991
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Clark, Paul T.
 - (B) REGISTRATION NUMBER: 30,162
 - (C) REFERENCE/DOCKET NUMBER: 00786/212001
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 542-5070
 - (B) TELEFAX: (617) 542-8906
 - (C) TELEX: 200154

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1728 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

TD4280" / E56E66D

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAACCGGG GAGTCCCTTT TAGGCACTTG CTTCTGGTGC TGCAACTGGC	50
GCTCCTCCCA GCAGCCACTC AGGGAAACAA AGTGGTGCTG GGCAAAAAAG	100
GGGATACAGT GGAAGTGACC TGTACAGCTT CCCAGAAGAA GAGCATACAA	150
TTCCACTGGA AAAACTCCAA CCAGATAAAG ATTCTGGGAA ATCAGGGGCTC	200
CTTCTTAACT AAAGGTCCAT CCAAGCTGAA TGATCGCGCT GACTCAAGAA	250
GAAGCCTTTG GGACCAAGGA AACTTCCCCC TGATCATCAA GAATCTTAAG	300
ATAGAAGACT CAGATACTTA CATCTGTGAA GTGGAGGACC AGAAGGAGGA	350
GGTGCAATTG CTAGTGTTCG GATTGACTGC CAACTCTGAC ACCCACCTGC	400
TTCAGGGGCA GAGCCTGACC CTGACCTTGG AGAGCCCCCC TGGTAGTAGC	450
CCCTCAGTGC AATGTAGGAG TCCAAGGGGT AAAACATAC AGGGGGGGAA	500
GACCTCTCC GTGTCTCAGC TGGAGCTCCA GGATAGTGGC ACCTGGACAT	550
GCACTGTCTT GCAGAACCAG AAGAAGGTGG AGTTCAAAAT AGACATCGTG	600
GTGCTAGCTT TCCAGAAGGC CTCCAGCATA GTCTATAAGA AAGAGGGGGA	650
ACAGGTGGAG TTCTCCTTCC CACTCGCCTT TACAGTTGAA AAGCTGACGG	700
GCAGTGGCGA GCTGTGGTGG CAGGCGGAGA GGGCTTCCTC CTCCAAGTCT	750
TGGATCACCT TTGACCTGAA GAACAAGGAA GTGTCTGTAA AACGGGTTAC	800
CCAGGACCCT AAGCTCCAGA TGGGCAAGAA GCTCCCGCTC CACCTCACCC	850
TGCCCCAGGC CTGCTCAG TATGCTGGCT CTGGAAACCT CACCCTGGCC	900
CTTGAAGCGA AAACAGGAAA GTTGATCAG GAAGTGAACC TGGTGGTGAT	950
GAGAGCCACT CAGCTCCAGA AAAATTTGAC CTGTGAGGTG TGGGGACCCA	1000
CCTCCCCTAA GCTGATGCTG AGCTTGAAC TGGAGAACAA GGAGGCAAAG	1050
GTCTCGAAGC GGGAGAAGCC GGTGTGGGTG CTGAACCCTG AGGCGGGGAT	1100
GTGGCAGTGT CTGCTGAGTG ACTCGGGACA GGTCTGTCTG GAATCCAACA	1150
TCAAGGTTCT GCCCACATGG TCCACCCCGG TGCACGCGGA TCCCAAATC	1200
TGCTACTTGC TAGATGGAAT CCTCTTCATC TACGGAGTCA TCATCACAGC	1250
CCTGTACCTG AGAGCAAAAT TCAGCAGGAG TGCAGAGACT GCTGCCAACC	1300
TGCAGGACCC CAACCAGCTC TACAATGAGC TCAATCTAGG GCGAAGAGAG	1350
GAATATGACG TCTTGGAGAA GAAGCGGGCT CGGGATCCAG AGATGGGAGG	1400
CAACAGCAG AGGAGGAGGA ACCCCCAGGA AGGCGTATAC AATGCACTGC	1450
AGAAAGACAA GATGCCAGAA GCCTACAGTG AGATCGGCAC AAAAGGCGAG	1500

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AGGCGGAGAG GCAAGGGGCA CGATGGCCTT TACCAGGACA GCCACTTCCA	1550
AGCAGTGCAG TTCGGGAACA GAAGAGAGAG AGAAGGTTCA GAACTCACAA	1600
GGACCCCTTG GTTAAGAGCC CGCCCCAAG GTGAAAGCAC CCAGCAGAGT	1650
AGCCAATCCT GTGCCAGCGT CTTCAGCATC CCCACTCTGT GGAGTCCATG	1700
GCCACCCAGT AGCAGCTCCC AGCTCTAA	1728

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGAACCGGG GAGTCCCTTT TAGGCACTTG CTTCTGGTGC TGCAACTGGC	50
GCTCCTCCCA GCAGCCACTC AGGGAAACAA AGTGGTGCTG GGCAAAAAG	100
GGGATACAGT GGAAGTGACC TGTACAGCTT CCCAGAAGAA GAGCATACAA	150
TTCCACTGGA AAAACTCCAA CCAGATAAAG ATTCTGGGAA ATCAGGGCTC	200
CTTCTTAACT AAAGGTCCAT CCAAGCTGAA TGATCGCGCT GACTCAAGAA	250
GAAGCCTTTG GGACCAAGGA AACTTCCCCC TGATCATCAA GAATCTTAAG	300
ATAGAAGACT CAGATACTTA CATCTGTGAA GTGGAGGACC AGAAGGAGGA	350
GGTGCAATTG CTAGTGTTCG GATTGACTGC CAACTCTGAC ACCCACCTGC	400
TTCAGGGGCA GAGCCTGACC CTGACCTTGG AGAGCCCCCC TGGTAGTAGC	450
CCCTCAGTGC AATGTAGGAG TCCAAGGGGT AAAACATAC AGGGGGGGAA	500
GACCCCTCTCC GTGTCTCAGC TGGAGCTCCA GGATAGTGGC ACCTGGACAT	550
GCACTGTCTT GCAGAACCAG AAGAAGGTGG AGTTCAAAAT AGACATCGTG	600
GTGCTAGCTT TCCAGAAGGC CTCCAGCATA GTCTATAAGA AAGAGGGGGA	650
ACAGGTGGAG TTCTCCTTCC CACTCGCCTT TACAGTTGAA AAGCTGACGG	700
GCAGTGGCGA GCTGTGGTGG CAGGCGGAGA GGGCTTCCTC CTCCAAGTCT	750
TGGATCACCT TTGACCTGAA GAACAAGGAA GTGTCTGTAA AACGGGTTAC	800
CCAGGACCCT AAGCTCCAGA TGGGCAAGAA GCTCCCGCTC CACCTCACCC	850
TGCCCCAGGC CTTGCCTCAG TATGCTGGCT CTGGAAACCT CACCCTGGCC	900
CTTGAAGCGA AAACAGGAAA GTTGCATCAG GAAGTGAACC TGGTGGTGAT	950

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GAGAGCCACT CAGCTCCAGA AAAATTGAC CTGTGAGGTG TGGGGACCCA	1000
CCTCCCCTAA GCTGATGCTG AGCTTGAAC TGGAGAACAA GGAGGCAAAG	1050
GTCTCGAAGC GGGAGAAGCC GGTGTGGGTG CTGAACCCTG AGGCGGGGAT	1100
GTGGCAGTGT CTGCTGAGTG ACTCGGGACA GGTCTGTCTG GAATCCAACA	1150
TCAAGGTTCT GCCCACATGG TCCACCCCGG TGCACGCGGA TCCGCAGCTC	1200
TGCTATATCC TGGATGCCAT CCTGTTTTTG TATGGTATTG TCCTTACCCT	1250
GCTCTACTGT CGACTCAAGA TCCAGGTCCG AAAGGCAGAC ATAGCCAGCC	1300
GTGAGAAATC AGATGCTGTC TACACGGGCG TGAACACCCG GAACCAGGAG	1350
ACATATGAGA CTCTGAAACA TGAGAAACCA CCCCAATAG	1389

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1599 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGAACCGGG GAGTCCCTTT TAGGCACTTG CTTCTGGTGC TGCAACTGGC	50
GCTCCTCCCA GCAGCCACTC AGGGAAACAA AGTGGTGCTG GGCAAAAAAG	100
GGGATACAGT GGAAC TGACCTG TGTACAGCTT CCCAGAAGAA GAGCATAACA	150
TTCCACTGGA AAAACTCCAA CCAGATAAAG ATTCTGGGAA ATCAGGGGCTC	200
CTTCTTAACT AAAGGTCCAT CCAAGCTGAA TGATCGCGCT GACTCAAGAA	250
GAAGCCTTTG GGACCAAGGA AACTTCCCCC TGATCATCAA GAATCTTAAG	300
ATAGAAGACT CAGATACTTA CATCTGTGAA GTGGAGGACC AGAAGGAGGA	350
GGTGCAATTG CTAGTGTTTG GATTGACTGC CAACTCTGAC ACCCACCTGC	400
TTCAGGGGCA GAGCCTGACC CTGACCTTGG AGAGCCCCCC TGGTAGTAGC	450
CCCTCAGTGC AATGTAGGAG TCCAAGGGGT AAAAACATAC AGGGGGGGAA	500
GACCCTCTCC GTGTCTCAGC TGGAGCTCCA GGATAGTGGC ACCTGGACAT	550
GCACTGTCTT GCAGAACCAG AAGAAGGTGG AGTTCAAAAT AGACATCGTG	600
GTGCTAGCTT TCCAGAAGGC CTCCAGCATA GTCTATAAGA AAGAGGGGGA	650
ACAGGTGGAG TTCTCCTTCC CACTCGCCTT TACAGTTGAA AAGCTGACGG	700
GCAGTGGCGA GCTGTGGTGG CAGGCGGAGA GGGCTTCCTC CTCCAAGTCT	750

TGGATCACCT TTGACCTGAA GAACAAGGAA GTGTCTGTAA AACGGGTTAC	800
CCAGGACCCT AAGCTCCAGA TGGGCAAGAA GCTCCCGCTC CACCTCACCC	850
TGCCCCAGGC CTTGCCTCAG TATGCTGGCT CTGGAAACCT CACCCTGGCC	900
CTTGAAGCGA AAACAGGAAA GTTGCAACAG GAAGTGAACC TGGTGGTGAT	950
GAGAGCCACT CAGCTCCAGA AAAATTTGAC CTGTGAGGTG TGGGGACCCA	1000
CCTCCCCCTAA GCTGATGCTG AGCTTGAAAC TGGAGAACAA GGAGGCAAAG	1050
GTCTCGAAGC GGGAGAAGCC GGTGTGGGTG CTGAACCCTG AGGCGGGGAT	1100
GTGGCAGTGT CTGCTGAGTG ACTCGGGACA GGTCTTGCTG GAATCCAACA	1150
TCAAGGTTCT GCCCACATGG TCCACCCCGG TGCACGCGGA TCCCAAATC	1200
TGCTACCTGC TGGATGGAAT CCTCTTCATC TATGGTGTC A TTCTCACTGC	1250
CTTGTTCTCTG AGAGTGAAGT TCAGCAGGAG CGCAGAGCCC CCCGCGTACC	1300
AGCAGGGCCA GAACCAGCTC TATAACGAGC TCAATCTAGG ACGAAGAGAG	1350
GAGTACGATG TTTTGGACAA GAGACGTGGC CGGGACCCTG AGATGGGGGG	1400
AAAGCCGAGA AGGAAGAACC CTCAGGAAGG CCTGTACAAT GAACTGCAGA	1450
AAGATAAGAT GCGGGAGGCC TACAGTGAGA TTGGGATGAA AGGCGAGCGC	1500
CGGAGGGGCA AGGGGCACGA TGGCCTTTAC CAGGGTCTCA GTACAGCCAC	1550
CAAGGACACC TACGACGCCC TTCACATGCA GGCCCTGCCC CCTCGCTAA	1599

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 575 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Asn	Arg	Gly	Val	Pro	Phe	Arg	His	Leu	Leu	Leu	Val	Leu	Gln	Leu
1				5					10					15	
Ala	Leu	Leu	Pro	Ala	Ala	Thr	Gln	Gly	Asn	Lys	Val	Val	Leu	Gly	Lys
			20					25					30		
Lys	Gly	Asp	Thr	Val	Glu	Leu	Thr	Cys	Thr	Ala	Ser	Gln	Lys	Lys	Ser
		35					40					45			
Ile	Gln	Phe	His	Trp	Lys	Asn	Ser	Asn	Gln	Ile	Lys	Ile	Leu	Gly	Asn
	50				55					60					
Gln	Gly	Ser	Phe	Leu	Thr	Lys	Gly	Pro	Ser	Lys	Leu	Asn	Asp	Arg	Ala
	65			70					75					80	
Asp	Ser	Arg	Arg	Ser	Leu	Trp	Asp	Gln	Gly	Asn	Phe	Pro	Leu	Ile	Ile
			85					90					95		
Lys	Asn	Leu	Lys	Ile	Glu	Asp	Ser	Asp	Thr	Tyr	Ile	Cys	Glu	Val	Gln
		100					105					110			
Asp	Gln	Lys	Glu	Glu	Val	Gln	Leu	Leu	Val	Phe	Gly	Leu	Thr	Ala	Asn
		115				120						125			

Ser	Asp	Thr	His	Leu	Leu	Gln	Gly	Gln	Ser	Leu	Thr	Leu	Thr	Leu	Glu
130						135						140			
Ser	Pro	Pro	Gly	Ser	Ser	Pro	Ser	Val	Gln	Cys	Arg	Ser	Pro	Arg	Gly
145					150					155					160
Lys	Asn	Ile	Gln	Gly	Gly	Lys	Thr	Leu	Ser	Val	Ser	Gln	Leu	Glu	Leu
				165					170						175
Gln	Asp	Ser	Gly	Thr	Trp	Thr	Cys	Thr	Val	Leu	Gln	Asn	Gln	Lys	Lys
			180					185					190		
Val	Glu	Phe	Lys	Ile	Asp	Ile	Val	Val	Leu	Ala	Phe	Gln	Lys	Ala	Ser
		195					200					205			
Ser	Ile	Val	Tyr	Lys	Lys	Glu	Gly	Glu	Gln	Val	Glu	Phe	Ser	Phe	Pro
	210					215					220				
Leu	Ala	Phe	Thr	Val	Glu	Lys	Leu	Thr	Gly	Ser	Gly	Glu	Leu	Trp	Trp
225					230					235					240
Gln	Ala	Glu	Arg	Ala	Ser	Ser	Ser	Lys	Ser	Trp	Ile	Thr	Phe	Asp	Leu
				245					250					255	
Lys	Asn	Lys	Glu	Val	Ser	Val	Lys	Arg	Val	Thr	Gln	Asp	Pro	Lys	Leu
			260					265					270		
Gln	Met	Gly	Lys	Lys	Leu	Pro	Leu	His	Leu	Thr	Leu	Pro	Gln	Ala	Leu
	275						280					285			
Pro	Gln	Tyr	Ala	Gly	Ser	Gly	Asn	Leu	Thr	Leu	Ala	Leu	Glu	Ala	Lys
	290					295					300				
Thr	Gly	Lys	Leu	His	Gln	Glu	Val	Asn	Leu	Val	Val	Met	Arg	Ala	Thr
305					310					315					320
Gln	Leu	Gln	Lys	Asn	Leu	Thr	Cys	Glu	Val	Trp	Gly	Pro	Thr	Ser	Pro
				325					330					335	
Lys	Leu	Met	Leu	Ser	Leu	Lys	Leu	Glu	Asn	Lys	Glu	Ala	Lys	Val	Ser
			340					345					350		
Lys	Arg	Glu	Lys	Pro	Val	Trp	Val	Leu	Asn	Pro	Glu	Ala	Gly	Met	Trp
	355						360					365			
Gln	Cys	Leu	Leu	Ser	Asp	Ser	Gly	Gln	Val	Leu	Leu	Glu	Ser	Asn	Ile
	370					375					380				
Lys	Val	Leu	Pro	Thr	Trp	Ser	Thr	Pro	Val	His	Ala	Asp	Pro	Lys	Leu
385					390					395					400
Cys	Tyr	Leu	Leu	Asp	Gly	Ile	Leu	Phe	Ile	Tyr	Gly	Val	Ile	Ile	Thr
				405					410					415	
Ala	Leu	Tyr	Leu	Arg	Ala	Lys	Phe	Ser	Arg	Ser	Ala	Glu	Thr	Ala	Ala
			420					425					430		
Asn	Leu	Gln	Asp	Pro	Asn	Gln	Leu	Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg
	435						440					445			
Arg	Glu	Glu	Tyr	Asp	Val	Leu	Glu	Lys	Lys	Arg	Ala	Arg	Asp	Pro	Glu
	450					455					460				
Met	Gly	Gly	Lys	Gln	Gln	Arg	Arg	Arg	Asn	Pro	Gln	Glu	Gly	Val	Tyr
465					470					475					480
Asn	Ala	Leu	Gln	Lys	Asp	Lys	Met	Pro	Glu	Ala	Tyr	Ser	Glu	Ile	Gly
			485						490					495	
Thr	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly	His	Asp	Gly	Leu	Tyr	Gln
			500					505					510		
Asp	Ser	His	Phe	Gln	Ala	Val	Gln	Phe	Gly	Asn	Arg	Arg	Glu	Arg	Glu
		515					520						525		
Gly	Ser	Glu	Leu	Thr	Arg	Thr	Leu	Gly	Leu	Arg	Ala	Arg	Pro	Lys	Gly
	530					535					540				
Glu	Ser	Thr	Gln	Gln	Ser	Ser	Gln	Ser	Cys	Ala	Ser	Val	Phe	Ser	Ile
555					550					565					560
Pro	Thr	Leu	Trp	Ser	Pro	Trp	Pro	Pro	Ser	Ser	Ser	Ser	Gln	Leu	
				565					570					575	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 462 amino acids

(ii) MOLECULE TYPE: protein

Met	Asn	Arg	Gly	Val	Pro	Phe	Arg	His	Leu	Leu	Val	Leu	Gln	Leu
1				5					10				15	
Ala	Leu	Leu	Pro	Ala	Ala	Thr	Gln	Gly	Asn	Lys	Val	Val	Leu	Gly
			20					25					30	Lys
Lys	Gly	Asp	Thr	Val	Glu	Leu	Thr	Cys	Thr	Ala	Ser	Gln	Lys	Lys
		35					40					45		Ser
Ile	Gln	Phe	His	Trp	Lys	Asn	Ser	Asn	Gln	Ile	Lys	Ile	Leu	Gly
	50				55						60			Asn
Gln	Gly	Ser	Phe	Leu	Thr	Lys	Gly	Pro	Ser	Lys	Leu	Asn	Asp	Arg
	65				70					75				Ala
Asp	Ser	Arg	Arg	Ser	Leu	Trp	Asp	Gln	Gly	Asn	Phe	Pro	Leu	Ile
			85						90					95
Lys	Asn	Leu	Lys	Ile	Glu	Asp	Ser	Asp	Thr	Tyr	Ile	Cys	Glu	Val
			100					105					110	Glu
Asp	Gln	Lys	Glu	Glu	Val	Gln	Leu	Leu	Val	Phe	Gly	Leu	Thr	Ala
		115					120					125		Asn
Ser	Asp	Thr	His	Leu	Leu	Gln	Gly	Gln	Ser	Leu	Thr	Leu	Thr	Leu
	130					135					140			Glu
Ser	Pro	Pro	Gly	Ser	Ser	Pro	Ser	Val	Gln	Cys	Arg	Ser	Pro	Arg
	145				150					155				Gly
Lys	Asn	Ile	Gln	Gly	Gly	Lys	Thr	Leu	Ser	Val	Ser	Gln	Leu	Glu
			165						170					Leu
Gln	Asp	Ser	Gly	Thr	Trp	Thr	Cys	Thr	Val	Leu	Gln	Asn	Gln	Lys
			180					185					190	Lys
Val	Glu	Phe	Lys	Ile	Asp	Ile	Val	Val	Leu	Ala	Phe	Gln	Lys	Ala
		195					200					205		Ser
Ser	Ile	Val	Tyr	Lys	Lys	Glu	Gly	Glu	Gln	Val	Glu	Phe	Ser	Phe
	210					215					220			Pro
Leu	Ala	Phe	Thr	Val	Glu	Lys	Leu	Thr	Gly	Ser	Gly	Glu	Leu	Trp
	225				230					235				Trp
Gln	Ala	Glu	Arg	Ala	Ser	Ser	Ser	Lys	Ser	Trp	Ile	Thr	Phe	Asp
			245						250					Leu
Lys	Asn	Lys	Glu	Val	Ser	Val	Lys	Arg	Val	Thr	Gln	Asp	Pro	Lys
		260						265					270	Leu
Gln	Met	Gly	Lys	Lys	Leu	Pro	Leu	His	Leu	Thr	Leu	Pro	Gln	Ala
	275						280					285		Leu
Pro	Gln	Tyr	Ala	Gly	Ser	Gly	Asn	Leu	Thr	Leu	Ala	Leu	Glu	Ala
	290					295					300			Lys
Thr	Gly	Lys	Leu	His	Gln	Glu	Val	Asn	Leu	Val	Val	Met	Arg	Ala
	305				310					315				Thr
Gln	Leu	Gln	Lys	Asn	Leu	Thr	Cys	Glu	Val	Trp	Gly	Pro	Thr	Ser
			325						330					Pro
Lys	Leu	Met	Leu	Ser	Leu	Lys	Leu	Glu	Asn	Lys	Glu	Ala	Lys	Val
		340						345					350	Ser
Lys	Arg	Glu	Lys	Pro	Val	Trp	Val	Leu	Asn					

(2) INFORMATION FOR SEQ ID NO:6:

(A) LENGTH: 532 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Asn	Arg	Gly	Val	Pro	Phe	Arg	His	Leu	Leu	Val	Leu	Gln	Leu		
1				5				10					15			
Ala	Leu	Leu	Pro	Ala	Ala	Thr	Gln	Gly	Asn	Lys	Val	Val	Leu	Gly	Lys	
			20					25					30			
Lys	Gly	Asp	Thr	Val	Glu	Leu	Thr	Cys	Thr	Ala	Ser	Gln	Lys	Lys	Ser	
			35				40					45				
Ile	Gln	Phe	His	Trp	Lys	Asn	Ser	Asn	Gln	Ile	Lys	Ile	Leu	Gly	Asn	
						55					60					
Gln	Gly	Ser	Phe	Leu	Thr	Lys	Gly	Pro	Ser	Lys	Leu	Asn	Asp	Arg	Ala	
						70				75					80	
Asp	Ser	Arg	Arg	Ser	Leu	Trp	Asp	Gln	Gly	Asn	Phe	Pro	Leu	Ile	Ile	
					85				90					95		
Lys	Asn	Leu	Lys	Ile	Glu	Asp	Ser	Asp	Thr	Tyr	Ile	Cys	Glu	Val	Glu	
					100			105					110			
Asp	Gln	Lys	Glu	Glu	Val	Gln	Leu	Leu	Val	Phe	Gly	Leu	Thr	Ala	Asn	
						120					125					
Ser	Asp	Thr	His	Leu	Leu	Gln	Gly	Gln	Ser	Leu	Thr	Leu	Thr	Leu	Glu	
						135					140					
Ser	Pro	Pro	Gly	Ser	Ser	Pro	Ser	Val	Gln	Cys	Arg	Ser	Pro	Arg	Gly	
					150				155						160	
Lys	Asn	Ile	Gln	Gly	Gly	Lys	Thr	Leu	Ser	Val	Ser	Gln	Leu	Gln	Leu	
					165				170					175		
Gln	Asp	Ser	Gly	Thr	Trp	Thr	Cys	Thr	Val	Leu	Gln	Asn	Gln	Lys	Lys	
					180			185					190			
Val	Glu	Phe	Lys	Ile	Asp	Ile	Val	Val	Leu	Ala	Phe	Gln	Lys	Ala	Ser	
							200				205					
Ser	Ile	Val	Tyr	Lys	Lys	Glu	Gly	Gln	Gln	Val	Glu	Phe	Ser	Phe	Pro	
						215					220					
Leu	Ala	Phe	Thr	Val	Glu	Lys	Leu	Thr	Gly	Ser	Gly	Glu	Leu	Trp	Trp	
					230				235					240		
Gln	Ala	Glu	Arg	Ala	Ser	Ser	Ser	Lys	Ser	Trp	Ile	Thr	Phe	Asp	Leu	
					245				250					255		
Lys	Asn	Lys	Glu	Val	Ser	Val	Lys	Arg	Val	Thr	Gln	Asp	Pro	Lys	Leu	
					260				265				270			
Gln	Met	Gly	Lys	Lys	Leu	Pro	Leu	His	Leu	Thr	Leu	Pro	Gln	Ala	Leu	
						280						285				
Pro	Gln	Tyr	Ala	Gly	Ser	Gly	Asn	Leu	Thr	Leu	Ala	Leu	Glu	Ala	Lys	
						295					300					
Thr	Gly	Lys	Leu	His	Gln	Glu	Val	Asn	Leu	Val	Val	Met	Arg	Ala	Thr	
					310					315					320	
Gln	Leu	Gln	Lys	Asn	Leu	Thr	Cys	Glu	Val	Trp	Gly	Pro	Thr	Ser	Pro	

Gln Cys Leu Leu Ser Asp Ser Gly Gln Val Leu Leu Glu Ser Asn Ile
 370 375 380
 Lys Val Leu Pro Thr Trp Ser Thr Pro Val His Ala Asp Pro Lys Leu
 385 390 395 400
 Cys Tyr Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly Val Ile Leu Thr
 405 410 415
 Ala Leu Phe Leu Arg Val Lys Phe Ser Arg Ser Ala Glu Pro Pro Ala
 420 425 430
 Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
 435 440 445
 Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
 450 455 460
 Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
 465 470 475 480
 Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
 485 490 495
 Lys Gly Glu Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
 500 505 510
 Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
 515 520 525
 Leu Pro Pro Arg
 530

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGCGGGGTGA CCGTCCCCTC CAGCAGCTTG GGC

33

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGCGGGGATC CGTCGTCCAG AGCCCCTCCA GCTCCCCGTC CTGGGCCTCA

50

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGCGGGCGGC CGCGACGCCG GCCAAGACAG CAC

33

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGCGTTGACG AGCAGCCAGT TGGGCAGCAG CAG

33

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGCGGGCGGC CGCTA

15

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGCGGGCTCG TTATAGAGCT GGTTCCTGGCG CTGCTTCTTC TG

42

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

FOR "JEEB" 056650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGCGGGGAGC TCGTTATAGA GCTGGTTTGC CGCCGAATTC TTATCCCG

48

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGCGGGGCGG CCACGCGTCC TCGCCAGCAC ACA

33

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGCGGGACGC GTTTCAGCCG TCCTCGCCAG CACACA

36

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGCGGGACGC GTGACCTGA GATGGGGGGA AAG

33

(2) INFORMATION FOR SEQ ID NO:17:

(A) LENGTH: 33 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

33

(A) LENGTH: 26 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

26

(A) LENGTH: 42 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

42

(A) LENGTH: 30 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

30

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCGGGGGCGG CCGCCTAAAT ACGGTTCTGG TC

32

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TCAGAAAGAG ACAACCTGAA GAAACCAACA A

31

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

TCAGAAAGAG ACAACCTGAA GAAACCAACA A

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TTGTTGGTTT CTTCAGGTTG TGTCTTCTG A

31

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 171 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Glu His Ser Thr Phe Leu Ser Gly Leu Val Leu Ala Thr Leu Leu
 5 10 15
 Ser Gln Val Ser Pro Phe Lys Ile Pro Ile Glu Glu Leu Glu Asp Arg
 20 25 30
 Val Phe Val Asn Cys Asn Thr Ser Ile Thr Trp Val Glu Gly Thr Val
 35 40 45
 Gly Thr Leu Leu Ser Asp Ile Thr Arg Leu Asp Leu Gly Lys Arg Ile
 50 55 60
 Leu Asp Pro Arg Gly Ile Tyr Arg Cys Asn Gly Thr Asp Ile Tyr Lys
 65 70 75 80
 Asp Lys Glu Ser Thr Val Gln Val His Tyr Arg Met Cys Gln Ser Cys
 85 90 95
 Val Glu Leu Asp Pro Ala Thr Val Ala Gly Ile Ile Val Thr Asp Val
 100 105 110
 Ala Ile Thr Leu Leu Leu Ala Leu Gly Val Phe Cys Phe Ala Gly His
 115 120 125
 Glu Thr Gly Arg Leu Ser Gly Ala Ala Asp Thr Gln Ala Leu Leu Arg
 130 135 140
 Asn Asp Gln Val Tyr Gln Pro Leu Arg Asp Arg Asp Ala Gln Tyr
 145 150 155 160
 Ser His Leu Gly Gly Asn Trp Ala Arg Asn Lys
 165 170

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 182 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Glu Gln Gly Lys Gly Leu Ala Val Leu Ile Leu Ala Ile Ile Leu
 5 10 15
 Leu Gln Gly Thr Leu Ala Gln Ser Ile Lys Gly Asn His Leu Val Lys
 20 25 30
 Val Tyr Asp Tyr Gln Glu Asp Gly Ser Val Leu Leu Thr Cys Asp Ala
 35 40 45
 Glu Ala Lys Asn Ile Thr Trp Phe Lys Asp Gly Lys Met Ile Gly Phe
 50 55 60

(ii) MOLECULE TYPE: amino acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

[illegible]